

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:53:29 ; Search time 118.5 Seconds

(without alignments)  
225.008 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gttctgctgcgttc 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/1/COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5/COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A/COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B/COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/H/COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/PCTUS/COMB.seq:\*
- 7: /cgn2\_6/prodata/1/ina/PP/COMB.seq:\*
- 8: /cgn2\_6/prodata/1/ina/RE/COMB.seq:\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	15	100.0	15	US-09-335-629-2
2	15	100.0	113	US-08-956-171E-4822
3	15	100.0	113	US-08-781-986A-4822
4	15	100.0	305	US-08-956-171E-4375
5	15	100.0	305	US-08-781-986A-4375
6	15	100.0	356	US-08-956-171E-4293
7	15	100.0	356	US-08-781-986A-4293
8	15	100.0	400	US-08-956-171E-3550
9	15	100.0	400	US-08-781-986A-3550
10	15	100.0	400	US-08-956-171E-3633
11	15	100.0	400	US-08-781-986A-3633
12	15	100.0	400	US-08-956-171E-3802
13	15	100.0	400	US-08-781-986A-3802
14	15	100.0	400	US-08-956-171E-4162
15	15	100.0	400	US-08-781-986A-4162
16	15	100.0	400	US-08-956-171E-3559
17	15	100.0	400	US-08-781-986A-3559
18	15	100.0	400	US-08-956-171E-3633
19	15	100.0	400	US-08-781-986A-3633
20	15	100.0	579	US-08-956-171E-1635
21	15	100.0	579	US-08-781-986A-1635
22	15	100.0	589	US-08-956-171E-3630
23	15	100.0	589	US-08-781-986A-3630
24	15	100.0	1171	US-08-956-171E-3539
				Sequence 2, Appli
				Sequence 4822, Ap
				Sequence 4822, Ap
				Sequence 4375, Ap
				Sequence 4375, Ap
				Sequence 4293, Ap
				Sequence 4293, Ap
				Sequence 3550, Ap
				Sequence 3559, Ap
				Sequence 3633, Ap
				Sequence 3802, Ap
				Sequence 3802, Ap
				Sequence 4162, Ap
				Sequence 3550, Ap
				Sequence 3559, Ap
				Sequence 3633, Ap
				Sequence 3802, Ap
				Sequence 3802, Ap
				Sequence 4162, Ap
				Sequence 1635, Ap
				Sequence 1635, Ap
				Sequence 3630, Ap
				Sequence 3630, Ap
				Sequence 3539, Ap

Sequence 3539, Ap	US-08-781-986A-3539	1171	100.0	15	C 25
Sequence 3194, Ap	US-08-956-171E-3194	1290	100.0	15	C 26
Sequence 3194, Ap	US-08-781-986A-3194	1290	100.0	15	C 27
Sequence 6, Appli	US-09-726-774-6	1484	100.0	15	C 28
Sequence 160, App	US-08-757-653-160	1555	100.0	15	C 29
Sequence 160, App	US-08-520-946-160	1555	100.0	15	C 30
Sequence 160, App	US-09-653-378A-160	1555	100.0	15	C 31
Sequence 3552, Ap	US-08-956-171E-3552	2209	100.0	15	C 32
Sequence 3552, Ap	US-08-781-986A-3552	2209	100.0	15	C 33
Sequence 56, Appli	US-08-956-171E-56	30246	100.0	15	C 34
Sequence 56, Appli	US-08-781-986A-56	30246	100.0	15	C 35
Sequence 4790, Ap	US-08-956-171E-4790	89.3	89.3	13.4	C 36
Sequence 4790, Ap	US-08-781-986A-4790	89.3	89.3	13.4	C 37
Sequence 8865, Ap	US-09-902-540-8865	609	89.3	13.4	C 38
Sequence 902, Ap	US-09-270-767-902	611	89.3	13.4	C 39
Sequence 16184, A	US-09-270-767-16184	611	89.3	13.4	C 40
Sequence 1, Appli	US-09-503-505A-1	1362	89.3	13.4	C 41
Sequence 14070, A	US-09-270-767-14070	1697	89.3	13.4	C 42
Sequence 9, Appli	US-08-693-103B-9	2556	89.3	13.4	C 43
Sequence 9, Appli	US-09-229-059-9	2556	89.3	13.4	C 44
Sequence 9, Appli	US-09-628-133-9	2556	89.3	13.4	C 45
Sequence 11, Appli	US-08-699-103B-11	2731	89.3	13.4	C 46
Sequence 11, Appli	US-09-229-059-11	2731	89.3	13.4	C 47
Sequence 11, Appli	US-09-628-133-11	2731	89.3	13.4	C 48
Sequence 9, Appli	US-08-747-562-9	2866	89.3	13.4	C 49
Sequence 2, Appli	US-09-503-505A-2	3497	89.3	13.4	C 50
Sequence 5817, Ap	US-09-949-016-5817	5492	89.3	13.4	C 51
Sequence 944, App	US-09-949-016-944	8540	89.3	13.4	C 52
Sequence 17556, A	US-09-949-016-17556	74644	89.3	13.4	C 53
Sequence 13973, A	US-09-270-767-13973	1121	86.7	13	C 54
Sequence 10, Appli	US-09-725-957-10	1319	86.7	13	C 55
Sequence 13, Appli	US-09-725-957-13	1344	86.7	13	C 56
Sequence 1242, Ap	US-09-902-540-1242	28783	86.7	13	C 57
Sequence 287, App	US-08-952-793-287	97	82.7	12.4	C 58
Sequence 287, App	US-09-849-928-287	97	82.7	12.4	C 59
Sequence 287, App	PCT-US96-00455A-287	97	82.7	12.4	C 60
Sequence 40, Appli	US-08-181-271A-40	340	82.7	12.4	C 61
Sequence 40, Appli	US-08-449-315-40	340	82.7	12.4	C 62
Sequence 40, Appli	US-08-444-803-40	340	82.7	12.4	C 63
Sequence 40, Appli	US-08-449-043-40	340	82.7	12.4	C 64
Sequence 40, Appli	US-08-456-265A-40	340	82.7	12.4	C 65
Sequence 40, Appli	US-08-455-416-40	340	82.7	12.4	C 66
Sequence 40, Appli	US-08-455-244-40	340	82.7	12.4	C 67
Sequence 40, Appli	US-08-454-876-40	340	82.7	12.4	C 68
Sequence 40, Appli	US-08-457-364-40	340	82.7	12.4	C 69
Sequence 40, Appli	US-08-456-262-40	340	82.7	12.4	C 70
Sequence 40, Appli	US-08-456-240-40	340	82.7	12.4	C 71
Sequence 40, Appli	US-08-455-736-40	340	82.7	12.4	C 72
Sequence 40, Appli	US-08-971-217-40	340	82.7	12.4	C 73
Sequence 40, Appli	US-09-350-600-40	340	82.7	12.4	C 74
Sequence 40, Appli	US-09-906-234-40	340	82.7	12.4	C 75
Sequence 19122, A	US-09-513-999C-19122	433	82.7	12.4	C 76
Sequence 19046, A	US-09-621-976-19046	462	82.7	12.4	C 77
Sequence 4834, Ap	US-09-533-559-4834	462	82.7	12.4	C 78
Sequence 26, Appli	US-09-975-316-26	493	82.7	12.4	C 79
Sequence 26, Appli	US-09-615-192A-26	508	82.7	12.4	C 80
Sequence 26, Appli	US-09-169-789-26	508	82.7	12.4	C 81
Sequence 26, Appli	US-09-270-767-28229	518	82.7	12.4	C 82
Sequence 1257, Ap	US-09-533-559-1257	588	82.7	12.4	C 83
Sequence 2593, Ap	US-09-533-559-2593	597	82.7	12.4	C 84
Sequence 70104, A	US-09-949-016-70104	601	82.7	12.4	C 85
Sequence 94191, A	US-09-949-016-94191	601	82.7	12.4	C 86
Sequence 16950, A	US-09-949-016-16950	601	82.7	12.4	C 87
Sequence 184368, A	US-09-949-016-184368	601	82.7	12.4	C 88
Sequence 205754, A	US-09-949-016-205754	601	82.7	12.4	C 89
Sequence 205755, A	US-09-949-016-205755	601	82.7	12.4	C 90
Sequence 205756, A	US-09-949-016-205756	601	82.7	12.4	C 91
Sequence 1176, Ap	US-09-107-532A-1176	618	82.7	12.4	C 92
Sequence 37, Appli	US-09-598-401C-37	648	82.7	12.4	C 93
Sequence 4547, Ap	US-09-533-559-4547	665	82.7	12.4	C 94
Sequence 4639, Ap	US-09-533-559-4639	678	82.7	12.4	C 95
Sequence 12849, A	US-09-270-767-12849	699	82.7	12.4	C 96
					C 97

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:41:34 ; Search time 1705.5 Seconds

(without alignments)  
411.496 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gcttcctgccttc 15

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

```
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	201	10	CG596662
2	15	100.0	229	10	CG670703
3	15	100.0	469	5	BW582202
4	15	100.0	486	5	BW574342
5	15	100.0	537	5	BW574342
6	15	100.0	661	9	BZ846224
7	15	100.0	672	6	CD427484
8	15	100.0	705	6	CB169687
9	15	100.0	718	6	CD462282
10	15	100.0	903	10	CNS01M9N
11	15	100.0	973	8	DR679944
12	15	100.0	1334	2	BG58140
13	15	100.0	1418	2	BF14115
14	14	93.3	86	6	CF003821
15	14	93.3	162	9	BZ712250
16	14	93.3	168	3	BZ683450
17	14	93.3	174	9	AZ086492
18	14	93.3	199	9	CC114390
19	14	93.3	264	5	BQ494805
20	14	93.3	269	9	AZ257720
21	14	93.3	298	1	AA793257
22	14	93.3	331	10	AG132185

C 23	14	93.3	359	5	BY173698
C 24	14	93.3	406	1	AA186624
C 25	14	93.3	407	3	BP526832
26	14	93.3	428	10	CZ114641
27	14	93.3	429	7	CV654226
28	14	93.3	451	2	BG489038
C 29	14	93.3	454	8	DR795082
C 30	14	93.3	469	10	AG268451
31	14	93.3	507	3	BJ534860
32	14	93.3	517	7	CV701467
33	14	93.3	521	1	AL929726
34	14	93.3	523	9	BH387066
C 35	14	93.3	523	9	BZ302204
C 36	14	93.3	526	10	AG976950
C 37	14	93.3	530	9	BH286581
C 38	14	93.3	535	3	BJ526748
C 39	14	93.3	542	11	FR0039013
C 40	14	93.3	552	9	AO512515
C 41	14	93.3	557	9	CC713154
C 42	14	93.3	570	10	AG971437
43	14	93.3	579	6	CF002582
C 44	14	93.3	606	2	BG532424
C 45	14	93.3	612	10	CE451613
46	14	93.3	615	6	CF017551
47	14	93.3	617	3	BJ024639
C 48	14	93.3	623	2	BE298920
C 49	14	93.3	632	11	DE039971
C 50	14	93.3	648	9	BH899238
51	14	93.3	651	10	CL972544
52	14	93.3	667	7	CK987950
53	14	93.3	675	6	CD650797
54	14	93.3	677	7	CV241577
55	14	93.3	680	8	DN586511
56	14	93.3	685	8	DN560688
57	14	93.3	685	10	CM013613
58	14	93.3	686	10	AG102835
59	14	93.3	709	8	CK724872
60	14	93.3	711	9	CC643278
C 61	14	93.3	712	3	BI872833
C 62	14	93.3	724	10	CG007385
C 63	14	93.3	725	7	CK186164
C 64	14	93.3	726	3	BI838675
C 65	14	93.3	729	10	CE270884
C 66	14	93.3	735	3	BI414805
67	14	93.3	741	3	BJ720211
68	14	93.3	756	9	BH666243
C 69	14	93.3	756	10	CG330968
C 70	14	93.3	782	10	CG268426
C 71	14	93.3	783	9	BZ733816
C 72	14	93.3	791	9	BH433362
C 73	14	93.3	796	9	BZ733812
74	14	93.3	798	9	BZ468768
C 75	14	93.3	799	9	BH899795
C 76	14	93.3	801	5	BU350535
C 77	14	93.3	805	11	CNS043V0
78	14	93.3	815	9	CC634234
C 79	14	93.3	817	9	CC695839
C 80	14	93.3	825	2	BE034274
C 81	14	93.3	841	2	BE283108
C 82	14	93.3	860	10	CG352157
C 83	14	93.3	862	9	CC610971
C 84	14	93.3	886	10	CG270251
C 85	14	93.3	893	11	CNS03281
86	14	93.3	899	10	AG841932
87	14	93.3	899	10	AG883216
C 88	14	93.3	906	2	BF302129
C 89	14	93.3	917	10	CG918274
C 90	14	93.3	912	10	AG902696
C 91	14	93.3	920	10	AG453826
C 92	14	93.3	923	9	CC408230
C 93	14	93.3	944	8	CV967263
94	14	93.3	945	9	CC408225
95	14	93.3	947	9	CC610979

AG132185 Pan trogl

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:40:39 ; Search time 902.5 Seconds  
(without alignments)  
944.767 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaaggagca 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.to.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	100.0	52	1	AF318151 Staphyloc
C 2	15	100.0	58	1	AF318162 Staphyloc
C 3	15	100.0	69	1	AF311730 Staphyloc
C 4	15	100.0	301	1	AF456354 Staphyloc
C 5	15	100.0	325	1	AF456348 Staphyloc
C 6	15	100.0	325	1	AF456349 Staphyloc
C 7	15	100.0	326	3	AF467317 Unculture
C 8	15	100.0	327	3	AF467310 Unculture
C 9	15	100.0	330	3	AF467318 Unculture
C 10	15	100.0	363	1	ULU78937
C 11	15	100.0	418	1	AF456351 Staphyloc
C 12	15	100.0	435	1	AF456352 Staphyloc
C 13	15	100.0	442	1	AY227283 Staphyloc
C 14	15	100.0	464	1	AY227263 Staphyloc
C 15	15	100.0	464	1	AY688054 Staphyloc
C 16	15	100.0	464	1	AY688055 Staphyloc
C 17	15	100.0	464	1	AY688056 Staphyloc
C 18	15	100.0	464	1	AY688091 Staphyloc

C 19	15	100.0	464	1	AY688092 Staphyloc
C 20	15	100.0	464	1	AY688093 Staphyloc
C 21	15	100.0	464	1	AY688094 Staphyloc
C 22	15	100.0	464	1	AY688102 Staphyloc
C 23	15	100.0	464	1	AY688103 Staphyloc
C 24	15	100.0	464	1	AY688107 Staphyloc
C 25	15	100.0	464	1	AY688108 Staphyloc
C 26	15	100.0	464	1	AY688109 Staphyloc
C 27	15	100.0	464	1	AY894722 Staphyloc
C 28	15	100.0	464	3	AF078296 Grassland
C 29	15	100.0	476	1	AY126224 Staphyloc
C 30	15	100.0	483	1	AY421711 Staphyloc
C 31	15	100.0	492	3	AY957696 Unculture
C 32	15	100.0	493	1	AY227255 Staphyloc
C 33	15	100.0	493	1	AY227257 Staphyloc
C 34	15	100.0	494	1	AY227261 Staphyloc
C 35	15	100.0	494	1	AY227264 Staphyloc
C 36	15	100.0	495	1	AY227258 Staphyloc
C 37	15	100.0	495	1	AY227260 Staphyloc
C 38	15	100.0	495	1	AY421709 Staphyloc
C 39	15	100.0	497	1	AY126181 Staphyloc
C 40	15	100.0	498	1	AY227276 Staphyloc
C 41	15	100.0	503	1	AY879102 Staphyloc
C 42	15	100.0	504	1	AF126240 Staphyloc
C 43	15	100.0	505	3	AF467319 Unculture
C 44	15	100.0	506	1	AY421710 Staphyloc
C 45	15	100.0	507	3	AF467321 Unculture
C 46	15	100.0	508	1	AY126191 Staphyloc
C 47	15	100.0	508	1	AY126199 Staphyloc
C 48	15	100.0	508	1	AY126241 Staphyloc
C 49	15	100.0	510	1	AY227256 Staphyloc
C 50	15	100.0	510	1	AY227262 Staphyloc
C 51	15	100.0	511	1	AY126197 Staphyloc
C 52	15	100.0	512	1	AY126183 Staphyloc
C 53	15	100.0	512	1	AY126184 Staphyloc
C 54	15	100.0	512	1	AY126185 Staphyloc
C 55	15	100.0	512	1	AY126246 Staphyloc
C 56	15	100.0	512	1	AY126259 Staphyloc
C 57	15	100.0	513	1	AY426179 Staphyloc
C 58	15	100.0	513	1	AY126187 Staphyloc
C 59	15	100.0	514	1	AY126177 Staphyloc
C 60	15	100.0	514	1	AY126186 Staphyloc
C 61	15	100.0	515	1	AY126192 Staphyloc
C 62	15	100.0	515	1	AY126195 Staphyloc
C 63	15	100.0	515	1	AY126247 Staphyloc
C 64	15	100.0	516	1	AY126188 Staphyloc
C 65	15	100.0	516	1	AY126190 Staphyloc
C 66	15	100.0	516	1	AY126236 Staphyloc
C 67	15	100.0	516	1	AY126248 Staphyloc
C 68	15	100.0	516	1	AY126249 Staphyloc
C 69	15	100.0	517	1	AY126176 Staphyloc
C 70	15	100.0	517	1	AY126178 Staphyloc
C 71	15	100.0	517	1	AY126180 Staphyloc
C 72	15	100.0	517	1	AY126193 Staphyloc
C 73	15	100.0	517	1	AY126239 Staphyloc
C 74	15	100.0	518	1	AY126194 Staphyloc
C 75	15	100.0	518	1	AY126235 Staphyloc
C 76	15	100.0	518	1	AY126237 Staphyloc
C 77	15	100.0	519	1	AY126196 Staphyloc
C 78	15	100.0	519	1	AY126238 Staphyloc
C 79	15	100.0	520	1	AY126251 Staphyloc
C 80	15	100.0	529	10	BV391692 S243P6148
C 81	15	100.0	553	3	AY437986 Unculture
C 82	15	100.0	594	1	SSP536446 Staphyloc
C 83	15	100.0	652	10	BV277977 S232P6127
C 84	15	100.0	668	1	AY526654 Staphyloc
C 85	15	100.0	685	3	AF467320 Unculture
C 86	15	100.0	698	3	AF467361 Unculture
C 87	15	100.0	750	2	AF483074 Boltenia
C 88	15	100.0	751	1	AY211101 Staphyloc
C 89	15	100.0	771	1	SE16SRNB
C 90	15	100.0	771	1	SS16SRND
C 91	15	100.0	1112	15	BT000079 Arabidops

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:40:39 ; Search time 902.5 Seconds  
(without alignments)  
944.767 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gctctcgctcgcttc 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883142 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	6	AR438392 Sequence
2	15	100.0	80	6	A32047 DNA probe (
3	15	100.0	80	6	A32065 DNA probe (
4	15	100.0	113	6	AR358704 Sequence
5	15	100.0	113	6	AR540260 Sequence
6	15	100.0	305	6	AR358257 Sequence
7	15	100.0	305	6	AR359813 Sequence
8	15	100.0	305	1	DQ056338 Sequence
9	15	100.0	356	6	AR358175 Sequence
10	15	100.0	356	6	AR359731 Sequence
11	15	100.0	400	6	AR357432 Sequence
12	15	100.0	400	6	AR357471 Sequence
13	15	100.0	400	6	AR357515 Sequence
14	15	100.0	400	6	AR357684 Sequence
15	15	100.0	400	6	AR357710 Sequence
16	15	100.0	400	6	AR358044 Sequence
17	15	100.0	400	6	AR358988 Sequence
18	15	100.0	400	6	AR539027 Sequence

AR539071	Sequence	400	6	AR539071	Sequence
AR539240	Sequence	400	6	AR539240	Sequence
AR539266	Sequence	400	6	AR539266	Sequence
AR539600	Sequence	400	6	AR539600	Sequence
AJ489358	Staphyloc	419	1	SSP489358	Staphyloc
AJ688031	Staphyloc	464	1	AY688031	Staphyloc
AY688032	Staphyloc	464	1	AY688032	Staphyloc
AY688033	Staphyloc	464	1	AY688033	Staphyloc
AY688034	Staphyloc	464	1	AY688034	Staphyloc
AY688035	Staphyloc	464	1	AY688035	Staphyloc
AJ295368	Rape rhiz	471	1	UBA295368	Rape rhiz
AJ295367	Rape rhiz	481	1	UBA295367	Rape rhiz
AJ266427	Marine ba	495	1	AY266427	Marine ba
AY939432	Unculture	503	3	AY939432	Unculture
AY126146	Staphyloc	505	3	AY126146	Staphyloc
AY939176	Unculture	505	3	AY939176	Unculture
AY939175	Unculture	506	3	AY939175	Unculture
AY939188	Unculture	506	3	AY939188	Unculture
AY939293	Unculture	506	3	AY939293	Unculture
AY939297	Unculture	506	3	AY939297	Unculture
AY939174	Unculture	507	3	AY939174	Unculture
AY939187	Unculture	507	3	AY939187	Unculture
AY939303	Unculture	507	3	AY939303	Unculture
AY939193	Unculture	508	3	AY939193	Unculture
AY939449	Unculture	508	3	AY939449	Unculture
AY939452	Unculture	509	3	AY939452	Unculture
AY126144	Staphyloc	510	1	AY126144	Staphyloc
AY939430	Unculture	510	3	AY939430	Unculture
AY939433	Unculture	510	3	AY939433	Unculture
AY939445	Unculture	510	3	AY939445	Unculture
AY939437	Unculture	511	3	AY939437	Unculture
AY939439	Unculture	511	3	AY939439	Unculture
AY939441	Unculture	511	3	AY939441	Unculture
AY939444	Unculture	511	3	AY939444	Unculture
AY939435	Unculture	512	3	AY939435	Unculture
AY939436	Unculture	513	3	AY939436	Unculture
AY939447	Unculture	513	3	AY939447	Unculture
AY939438	Unculture	514	3	AY939438	Unculture
AY126148	Staphyloc	515	1	AY126148	Staphyloc
AY304999	Staphyloc	515	1	AY305000S2	Staphyloc
AY126147	Staphyloc	516	1	AY126147	Staphyloc
AY126145	Staphyloc	517	1	AY126145	Staphyloc
AY504461	Staphyloc	525	1	AY504461	Staphyloc
AR535517	Sequence	529	6	AR535517	Sequence
AR537073	Sequence	579	6	AR537073	Sequence
AR357512	Sequence	589	6	AR357512	Sequence
AR539068	Sequence	589	6	AR539068	Sequence
AJ330262	Homo sapi	747	8	HA330262	Homo sapi
AF343958	Staphyloc	757	1	AF343958	Staphyloc
Z26896	S.haemolyti	771	1	SH16SRNRD	S.haemolyti
AY805987	Unculture	798	3	AY805987	Unculture
AY805992	Unculture	799	3	AY805992	Unculture
AY806277	Unculture	799	3	AY806277	Unculture
AY806472	Unculture	807	3	AY806472	Unculture
AY806200	Unculture	816	3	AY806200	Unculture
AY806674	Unculture	816	3	AY806674	Unculture
AY807213	Unculture	834	3	AY807213	Unculture
AY807396	Unculture	834	3	AY807396	Unculture
AY437618	Staphyloc	840	1	AY437618	Staphyloc
AY807545	Unculture	849	3	AY807545	Unculture
AY807542	Unculture	850	3	AY807542	Unculture
AY807554	Unculture	861	3	AY807554	Unculture
AY807387	Unculture	870	3	AY807387	Unculture
AY859409	Staphyloc	958	1	AY859409	Staphyloc
AF076030	Staphyloc	1141	1	AF076030	Staphyloc
AR357421	Sequence	1171	6	AR357421	Sequence
AR538977	Sequence	1171	6	AR538977	Sequence
AR357076	Sequence	1290	6	AR357076	Sequence
AR538632	Sequence	1290	6	AR538632	Sequence
SA16S	Sequence	1437	1	SA16S	Sequence
AF015929	Staphyloc	1442	1	AF015929	Staphyloc
STAL6SRR01	Staphyloc	1476	1	STAL6SRR01	Staphyloc
STAL6SRR02	Staphyloc	1476	1	STAL6SRR02	Staphyloc

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:39:02 ; Search time 244.5 Seconds  
(without alignments)  
408.877 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gcttcgctccgttc 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : N Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	12	Adm86613 S. aureus
2	15	100.0	15	14	Adx26645 Probe A f
3	15	100.0	15	14	Aea89581 Staphyloc
4	15	100.0	15	14	Adx26648 Staphyloc
5	15	100.0	43	14	Adx26654 Staphyloc
6	15	100.0	43	14	Adx26653 Staphyloc
7	15	100.0	50	12	Adf94003 Microorga
8	15	100.0	113	2	AAV79133
9	15	100.0	305	2	AAV78686
10	15	100.0	356	2	AAV78604
11	15	100.0	360	13	ADV99473
12	15	100.0	400	2	AAV78473
13	15	100.0	400	2	AAV77944
14	15	100.0	400	2	AAV78113
15	15	100.0	400	2	AAV77861
16	15	100.0	400	2	AAV78139
17	15	100.0	400	2	AAV77900
18	15	100.0	579	2	AAV75946
19	15	100.0	589	2	AAV77941

C	20	15	100.0	1171	2	AAV77850	Aav77850 Staphyloc
C	21	15	100.0	1239	13	ADS48229	AdS48229 Bacterial
C	22	15	100.0	1290	2	AAV77505	Aav77505 Staphyloc
C	23	15	100.0	1442	6	ABS71606	Abs71606 Staphyloc
C	24	15	100.0	1484	5	AAS11026	Aas11026 Staphyloc
C	25	15	100.0	1555	2	AAT29142	Aat29142 rRNA gene
C	26	15	100.0	1555	2	AAV24294	Aav24294 Staphyloc
C	27	15	100.0	1555	6	AKX99056	Akx99056 DNA of th
C	28	15	100.0	1555	6	AKX99099	Akx99099 DNA encod
C	29	15	100.0	1555	9	ADB16301	Adb16301 Cleavase
C	30	15	100.0	1555	10	ADB61676	Adb61676 16S rRNA
C	31	15	100.0	1555	10	ADC02549	Adc02549 S. aureus
C	32	15	100.0	1555	14	ADM94447	Adm94447 Prolifera
C	33	15	100.0	1555	14	ADM94575	Adm94575 Prolifera
C	34	15	100.0	1555	14	ADM94604	Adm94604 Prolifera
C	35	15	100.0	1555	14	ADM94509	Adm94509 Prolifera
C	36	15	100.0	2209	2	AAV77863	Aav77863 Staphyloc
C	37	15	100.0	5029	14	ADM94255	Adm94255 Staphyloc
C	38	15	100.0	5134	14	ADM94228	Adm94228 Staphyloc
C	39	15	100.0	5648	14	ADM94202	Adm94202 Staphyloc
C	40	15	100.0	7291	14	ADM94182	Adm94182 Staphyloc
C	41	15	100.0	30246	2	AAV74367	Aav74367 Staphyloc
C	42	14	93.3	19	12	ADO18380	Ado18380 Analytica
C	43	14	93.3	19	12	ADO18671	Ado18671 Analytica
C	44	14	93.3	19	12	ADO18243	Ado18243 Analytica
C	45	14	93.3	19	12	ADO18529	Ado18529 Analytica
C	46	14	93.3	24	3	AAZ24183	Aaz24183 Bacterial
C	47	14	93.3	24	3	AAZ24171	Aaz24171 Bacterial
C	48	14	93.3	589	10	ADK55636	Adk55636 Plant DNA
C	49	14	93.3	649	10	ADK59378	Adk59378 Plant DNA
C	50	14	93.3	939	8	ACA47616	ACA47616 Prokaryot
C	51	14	93.3	1014	13	ADT16297	Adt16297 Plant CDN
C	52	14	93.3	1290	4	AAZ56287	Aaz56287 Salmoneil
C	53	14	93.3	1290	8	ACA52051	ACA52051 Prokaryot
C	54	14	93.3	1290	8	ACA51053	ACA51053 Prokaryot
C	55	14	93.3	1500	10	ADK60148	Adk60148 Plant DNA
C	56	14	93.3	1593	4	ABL25547	AbL25547 Drosophil
C	57	14	93.3	2744	13	ADS54871	Ads54871 Bacterial
C	58	14	93.3	2744	13	ADS54872	Ads54872 Bacterial
C	59	14	93.3	3774	4	ABL25546	AbL25546 Drosophil
C	60	13.4	89.3	25	9	ACI73669	ACI73669 Human mic
C	61	13.4	89.3	43	14	ADX26652	Adx26652 Staphyloc
C	62	13.4	89.3	43	14	ADX26651	Adx26651 Staphyloc
C	63	13.4	89.3	43	14	ADX26647	Adx26647 Staphyloc
C	64	13.4	89.3	129	2	AAV79101	Aav79101 Staphyloc
C	65	13.4	89.3	303	12	ADJ71864	Adj71864 Human DNA
C	66	13.4	89.3	303	12	ADJ71861	Adj71861 Human DNA
C	67	13.4	89.3	303	12	ADJ71865	Adj71865 Human DNA
C	68	13.4	89.3	303	12	ADJ71863	Adj71863 Human DNA
C	69	13.4	89.3	449	9	ACH39588	Ach39588 Human foe
C	70	13.4	89.3	538	6	ABZ34920	Abz34920 Human gen
C	71	13.4	89.3	587	6	ABZ34920	Abz34920 Human gen
C	72	13.4	89.3	609	14	ACL72402	ACL72402 M. xanthu
C	73	13.4	89.3	763	3	AAC39828	Aac39828 Arabidops
C	74	13.4	89.3	807	4	ABL30209	AbL30209 Drosophil
C	75	13.4	89.3	855	13	ADT42391	Adt42391 Bacterial
C	76	13.4	89.3	1014	10	ADG73022	Adg73022 DNA encod
C	77	13.4	89.3	1014	10	ADL12077	Adl12077 Pseudomon
C	78	13.4	89.3	1056	6	ABK75036	Abk75036 Bacillus
C	79	13.4	89.3	1101	12	ADJ71868	Adj71868 Human DNA
C	80	13.4	89.3	1116	12	ADJ71867	Adj71867 Human DNA
C	81	13.4	89.3	1134	12	ADJ71866	Adj71866 Human DNA
C	82	13.4	89.3	1167	12	ADJ71869	Adj71869 Human DNA
C	83	13.4	89.3	1179	12	ADJ71872	Adj71872 Human DNA
C	84	13.4	89.3	1179	12	ADJ71871	Adj71871 Human DNA
C	85	13.4	89.3	1179	12	ADJ71862	Adj71862 Human DNA
C	86	13.4	89.3	1179	12	ADJ71870	Adj71870 Human DNA
C	87	13.4	89.3	1197	13	ADS47832	Ads47832 Bacterial
C	88	13.4	89.3	1221	13	ADT45063	Adt45063 Bacterial
C	89	13.4	89.3	1260	8	ACA24877	Aca24877 Prokaryot
C	90	13.4	89.3	1341	6	ABQ69254	Abq69254 Listeria
C	91	13.4	89.3	1356	6	ABQ67804	Abq67804 Listeria
C	92	13.4	89.3	1362	3	AAA59628	Aaa59628 Nucleotid

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:15:47 ; Search time 282 Seconds  
(without alignments)  
116.622 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gctctgcgttc 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 500 summaries

#### Database :

Published Applications NA New:

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US12\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US13\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US14\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US15\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US16\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US17\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US18\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-10-631-289-2	Sequence 2, Appli
C 2	15	100.0	1555	US-11-198-746-160	Sequence 160, App
C 3	15	100.0	1555	US-11-198-794-160	Sequence 160, App
C 4	15	100.0	1555	US-11-198-857-160	Sequence 160, App
C 5	13.4	89.3	568	US-09-925-065A-751129	Sequence 751129,
C 6	13.4	89.3	600	US-10-750-185-2543	Sequence 2543, Ap
C 7	13.4	89.3	600	US-10-750-623-2543	Sequence 2543, Ap
C 8	13.4	89.3	793	US-10-750-185-43321	Sequence 43321, A
C 9	13.4	89.3	793	US-10-750-623-43321	Sequence 43321, A
C 10	13.4	89.3	2727	US-10-821-234-415	Sequence 415, Appl
C 11	13.4	89.3	5259	US-11-181-330-1	Sequence 31, Appl
C 12	13.4	89.3	5382	US-11-136-527-2050	Sequence 2050, Ap
C 13	13.4	89.3	6126	US-10-775-169-286	Sequence 286, App
C 14	13.4	89.3	14896	US-11-000-147-243	Sequence 243, App
C 15	13.4	89.3	14896	US-11-000-688-946	Sequence 946, Appl
C 16	13.4	89.3	14896	US-11-076-427A-31	Sequence 31, Appl
C 17	13.4	89.3	173120	US-11-114-798-55	Sequence 55, Appl
C 18	13.4	89.3	182303	US-11-121-086-45	Sequence 45, Appl
C 19	13	86.7	548	US-09-925-065A-46850	Sequence 46850, A
C 20	13	86.7	80345	US-11-124-367A-5022	Sequence 5022, Ap

13	86.7	81706	8	US-10-995-561-13417	Sequence 13417, A
13	86.7	1125000	8	US-10-995-561-13286	Sequence 13286, A
22	82.7	50	12	US-11-175-859-28227	Sequence 28227, A
23	82.7	86	6	US-10-310-914A-13940	Sequence 13940, A
24	82.7	326	6	US-09-925-065A-448010	Sequence 448010,
C 25	82.7	336	6	US-09-925-065A-797025	Sequence 797025,
C 26	82.7	336	6	US-09-925-065A-850758	Sequence 850758,
C 27	82.7	363	6	US-09-925-065A-638012	Sequence 638012,
C 28	82.7	409	6	US-09-925-065A-795181	Sequence 795181,
C 29	82.7	415	6	US-11-136-527-15	Sequence 15, Appl
C 30	82.7	417	12	US-11-136-527-4111	Sequence 4111, Ap
C 31	82.7	417	12	US-09-925-065A-850759	Sequence 850759,
C 32	82.7	419	6	US-09-925-065A-448011	Sequence 448011,
C 33	82.7	429	6	US-09-925-065A-448008	Sequence 448008,
C 34	82.7	458	6	US-09-925-065A-124697	Sequence 124697,
C 35	82.7	485	6	US-09-925-065A-954872	Sequence 954872,
C 36	82.7	492	6	US-09-925-065A-543499	Sequence 543499,
C 37	82.7	494	6	US-09-925-065A-795180	Sequence 795180,
C 38	82.7	494	6	US-09-925-065A-795182	Sequence 795182,
C 39	82.7	494	6	US-09-925-065A-851789	Sequence 851789,
C 40	82.7	494	6	US-09-925-065A-946592	Sequence 946592,
C 41	82.7	495	6	US-09-925-065A-850757	Sequence 850757,
C 42	82.7	503	6	US-09-925-065A-797024	Sequence 797024,
C 43	82.7	510	6	US-09-925-065A-797026	Sequence 797026,
C 44	82.7	510	6	US-09-925-065A-111308	Sequence 111308,
C 45	82.7	511	6	US-09-925-065A-232256	Sequence 232256,
C 46	82.7	517	6	US-09-925-065A-665062	Sequence 665062,
C 47	82.7	533	6	US-09-925-065A-435304	Sequence 435304,
C 48	82.7	554	6	US-09-925-065A-316047	Sequence 316047,
C 49	82.7	566	6	US-09-925-065A-404249	Sequence 404249,
C 50	82.7	570	6	US-09-925-065A-232257	Sequence 232257,
C 51	82.7	570	6	US-09-925-065A-448012	Sequence 448012,
C 52	82.7	572	6	US-09-925-065A-108088	Sequence 108088,
C 53	82.7	585	6	US-09-925-065A-787292	Sequence 787292,
C 54	82.7	586	6	US-09-925-065A-813086	Sequence 813086,
C 55	82.7	586	6	US-09-925-065A-341380	Sequence 341380,
C 56	82.7	589	6	US-09-925-065A-939583	Sequence 939583,
C 57	82.7	596	6	US-09-925-065A-921523	Sequence 921523,
C 58	82.7	596	6	US-09-925-065A-921524	Sequence 921524,
C 59	82.7	603	6	US-09-925-065A-444395	Sequence 444395,
C 60	82.7	606	6	US-09-925-065A-444396	Sequence 444396,
C 61	82.7	606	6	US-09-925-065A-795609	Sequence 795609,
C 62	82.7	632	6	US-09-925-065A-6710	Sequence 6710, Ap
C 63	82.7	632	6	US-09-925-065A-6711	Sequence 6711, Ap
C 64	82.7	632	6	US-09-925-065A-6712	Sequence 6712, Ap
C 65	82.7	637	6	US-09-925-065A-6713	Sequence 6713, Ap
C 66	82.7	646	6	US-10-927-641-37	Sequence 37, Appl
C 67	82.7	646	6	US-09-925-065A-801292	Sequence 801292,
C 68	82.7	646	6	US-09-925-065A-801293	Sequence 801293,
C 69	82.7	646	6	US-09-925-065A-801294	Sequence 801294,
C 70	82.7	646	6	US-09-925-065A-850590	Sequence 850590,
C 71	82.7	646	6	US-09-925-065A-112693	Sequence 112693,
C 72	82.7	662	6	US-09-925-065A-680454	Sequence 680454,
C 73	82.7	662	6	US-09-925-065A-782688	Sequence 782688,
C 74	82.7	662	6	US-10-750-185-56409	Sequence 56409, A
C 75	82.7	662	6	US-10-750-623-56409	Sequence 56409, A
C 76	82.7	662	6	US-09-925-065A-17024	Sequence 17024, A
C 77	82.7	662	6	US-09-925-065A-17025	Sequence 17025, A
C 78	82.7	662	6	US-09-925-065A-17026	Sequence 17026, A
C 79	82.7	662	6	US-09-925-065A-84823	Sequence 84823, A
C 80	82.7	662	6	US-10-750-185-35055	Sequence 35055, A
C 81	82.7	662	6	US-10-750-623-35055	Sequence 35055, A
C 82	82.7	662	6	US-10-750-185-45107	Sequence 45107, A
C 83	82.7	662	6	US-10-750-623-45107	Sequence 45107, A
C 84	82.7	662	6	US-10-750-185-29185	Sequence 29185, A
C 85	82.7	662	6	US-10-750-623-29185	Sequence 29185, A
C 86	82.7	662	6	US-11-076-733-17	Sequence 17, Appl
C 87	82.7	662	6	US-09-925-065A-43144	Sequence 43144, A
C 88	82.7	662	6	US-09-925-065A-43145	Sequence 43145, A

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:12:03 ; Search time 401.5 Seconds  
(without alignments)  
308.943 Million cell updates

Title: US-10-804-470-1

Perfect score:

Sequence: 1 gcttctcgctccgttc 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

```
Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07
2: /cgn2_6/ptodata/1/pubpna/US08
3: /cgn2_6/ptodata/1/pubpna/US09
4: /cgn2_6/ptodata/1/pubpna/US09a
5: /cgn2_6/ptodata/1/pubpna/US10
6: /cgn2_6/ptodata/1/pubpna/US10a
7: /cgn2_6/ptodata/1/pubpna/US10b
8: /cgn2_6/ptodata/1/pubpna/US10c
9: /cgn2_6/ptodata/1/pubpna/US10d
10: /cgn2_6/ptodata/1/pubpna/US10e
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	15	100.0	15	8	US-10-804-470-1
2	15	100.0	43	8	US-10-804-470-4
3	15	100.0	43	8	US-10-804-470-9
4	15	100.0	43	8	US-10-804-470-10
5	15	100.0	113	2	US-08-781-986A-4822
6	15	100.0	113	7	US-10-329-624-4822
7	15	100.0	305	2	US-08-781-986A-4375
8	15	100.0	305	7	US-10-329-624-4375
9	15	100.0	356	2	US-08-781-986A-4293
10	15	100.0	356	7	US-10-329-624-4293
11	15	100.0	400	2	US-08-781-986A-3550
12	15	100.0	400	2	US-08-781-986A-3589
13	15	100.0	400	2	US-08-781-986A-3633
14	15	100.0	400	2	US-08-781-986A-3802
15	15	100.0	400	2	US-08-781-986A-3828
16	15	100.0	400	2	US-08-781-986A-4162
17	15	100.0	400	7	US-10-329-624-3550
18	15	100.0	400	7	US-10-329-624-3589
19	15	100.0	400	7	US-10-329-624-3633
20	15	100.0	400	7	US-10-329-624-3802
21	15	100.0	400	7	US-10-329-624-3828
22	15	100.0	400	7	US-10-329-624-4162
23	15	100.0	579	2	US-08-781-986A-1635

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:39:02 ; Search time 244.5 Seconds  
(without alignments)  
408.877 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaaggagcaaa 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

N\_Geneseq\_21.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2002as.\*

6: Geneseqn2002bs.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2003ds.\*

11: Geneseqn2004as.\*

12: Geneseqn2004bs.\*

13: Geneseqn2004cs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	14	ADx26646
2	15	100.0	43	14	ADx26652
3	15	100.0	43	14	ADx26651
4	15	100.0	43	14	ADx26649
5	15	100.0	43	14	ADx26647
6	15	100.0	43	14	ADx26650
7	15	100.0	1122	3	AAC36196
8	15	100.0	1234	3	AAC37820
9	15	100.0	2102	4	AAI68993
10	14	93.3	41	2	AAV39906
11	14	93.3	41	6	ABO85067
12	14	93.3	41	10	ADC45470
13	14	93.3	172	3	AAC31883
14	14	93.3	223	5	AAC33655
15	14	93.3	339	9	ADA32201
16	14	93.3	373	5	ABV17168
17	14	93.3	378	8	ABX42264
18	14	93.3	434	5	ADI72025
19	14	93.3	434	5	ADL37174

20	14	93.3	503	5	ABV46963
21	14	93.3	523	10	ADE78377
22	14	93.3	525	10	ADE78378
23	14	93.3	578	5	AAS34736
24	14	93.3	578	5	AAS34737
25	14	93.3	578	5	AAS34738
26	14	93.3	585	5	ADL43558
27	14	93.3	784	2	AAV27405
28	14	93.3	784	6	ABQ84873
29	14	93.3	784	10	ADC45244
30	14	93.3	794	13	ADN33184
31	14	93.3	981	13	ADT20022
32	14	93.3	1116	6	ABN90844
33	14	93.3	1116	13	ADS00985
34	14	93.3	1134	13	ADR93082
35	14	93.3	1134	13	ADK46071
36	14	93.3	1134	14	AEA56952
37	14	93.3	1230	13	ADN33185
38	14	93.3	1410	6	ABN81334
39	14	93.3	1410	8	ABX16241
40	14	93.3	1689	10	ABX06328
41	14	93.3	1692	3	AAA05463
42	14	93.3	1693	3	AAO05462
43	14	93.3	2147	14	ABE67769
44	14	93.3	2188	12	ADN05369
45	14	93.3	3068	13	ADT19986
46	14	93.3	3135	2	AAV82049
47	14	93.3	3135	2	AAV82048
48	14	93.3	3135	2	AAV16687
49	14	93.3	3135	2	AAV16688
50	14	93.3	3135	4	AAH47451
51	14	93.3	3135	4	AAH47452
52	14	93.3	3135	9	ADA14564
53	14	93.3	3135	9	ADA14561
54	14	93.3	4008	4	ABL20178
55	14	93.3	4085	14	AEA22587
56	14	93.3	4085	14	ABE86304
57	14	93.3	4174	6	ABZ35297
58	14	93.3	4345	5	AAH86250
59	14	93.3	4361	10	ABT42027
60	14	93.3	4361	12	ADP72826
61	14	93.3	5034	12	ADP76091
62	14	93.3	5217	4	ABL21514
63	14	93.3	5554	12	ADN04185
64	14	93.3	5555	6	ABZ35675
65	14	93.3	6317	8	ACC47865
66	14	93.3	10785	4	ABA07367
67	14	93.3	10785	4	AAK91098
68	14	93.3	10785	4	AAK65411
69	14	93.3	10785	5	AAH30060
70	14	93.3	10785	10	ADB33397
71	14	93.3	12729	5	AAF97873
72	14	93.3	13315	4	ABA07371
73	14	93.3	13315	4	AAK91102
74	14	93.3	13315	4	AAK65415
75	14	93.3	13315	5	AAH30064
76	14	93.3	13315	10	ADB33401
77	14	93.3	13926	2	AAV52138
78	14	93.3	20261	4	ABA07368
79	14	93.3	20261	4	AAK91099
80	14	93.3	20261	4	AAK65412
81	14	93.3	20261	5	AAH30061
82	14	93.3	20261	10	ADB33398
83	14	93.3	25464	2	AAV57274
84	14	93.3	84805	14	ABE39165
85	14	93.3	110000	10	ADE11169
86	14	93.3	110000	10	ABE56454
87	14	93.3	110000	10	ABE39175
88	14	93.3	110000	14	ABE42401
89	14	93.3	110000	14	ABE42736
90	14	93.3	125910	3	AC64370
91	14	93.3	150351	13	ABD33360
92	14	93.3	185548	13	ADV34986

ABV46963	Human pro
Ade78377	Endometri
Ade78378	Endometri
Aas34736	Human DNA
Aas34737	Human DNA
Aas34738	Human DNA
Adl43558	Human ova
AAV27405	Streptoco
ABQ84873	S. pneumo
ADC45244	S. pneumo
ADN33184	Human tra
ADT20022	Plant cdn
ABN90844	Staphyloc
ADS00985	Staphyloc
ADR93082	Novel S.
ADK46071	Streptoco
AEA56952	Streptoco
ADN33185	Human tra
ABN81334	Physcomit
ABX16241	P. patens
ABX06328	S. pneumo
AAA05463	Streptoco
AAO05462	Streptoco
ABE67769	Rice geno
ADN05369	Antipsori
ADT19986	Plant cdn
AAV82049	Polynucle
AAV82048	S. pneumo
AAV16687	Streptoco
AAV16688	Streptoco
AAH47451	S. pneumo
AAH47452	S. pneumo
ADA14564	DNA encod
ADA14561	DNA encod
ABL20178	Drosophila
AEA22587	TRP chann
ABE86304	Nucleotid
ABZ35297	Human gen
AAH86250	DNA encod
ABT42027	Toxicity
ADP72826	Renal tox
ADP76091	Genomic D
ABL21514	Drosophila
ADN04185	Antipsori
ABZ35675	Human gen
ACC47865	P. obesus
ABA07367	Human pan
AAK91098	Human dig
AAK65411	Human imm
AAH30060	Human lun
ADB33397	Human neu
AAF97873	Human pan
ABA07371	Human pan
AAK91102	Human dig
AAK65415	Human imm
AAH30064	Human lun
ADB33401	Human nov
AAV52138	Streptoco
ABA07368	Human pan
AAK91099	Human dig
AAK65412	Human imm
AAH30061	Human lun
ADB33398	Human nov
AAV57274	Human fla
ABE39165	L. pneumo
ADE11169	Continuation (3 of
ABE56454	Continuation (6 of
ABE39175	Continuation (7 of
ABE42401	Continuation (7 of
ABE42736	L. pneumo
AC64370	Human KCN
ABD33360	Murine ca
ADV34986	Murine cd



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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:53:29 ; Search time 118.5 Seconds  
(without alignments)  
225.008 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaagagagcaa 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/PCUS COMB.seq.\*
- 7: /cgn2\_6/prodata/1/ina/pp COMB.seq.\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	14	93.3	41	US-08-961-083-389
C 2	14	93.3	41	US-09-536-784-389
C 3	14	93.3	41	US-09-765-271-389
C 4	14	93.3	41	US-09-765-272A-389
C 5	14	93.3	172	US-09-513-999C-25958
C 6	14	93.3	339	US-09-328-352-3488
C 7	14	93.3	601	US-09-949-016-27145
C 8	14	93.3	601	US-09-949-016-63597
C 9	14	93.3	601	US-09-949-016-63598
C 10	14	93.3	784	US-08-961-083-163
C 11	14	93.3	784	US-09-536-784-163
C 12	14	93.3	784	US-09-765-271-163
C 13	14	93.3	784	US-09-765-272A-163
C 14	14	93.3	1116	US-09-134-001C-307
C 15	14	93.3	1134	US-09-583-110-2586
C 16	14	93.3	1134	US-09-583-110-2586
C 17	14	93.3	1134	US-09-107-433-1117
C 18	14	93.3	1410	US-09-828-302-10
C 19	14	93.3	1692	US-09-769-787-235
C 20	14	93.3	1692	US-09-769-787-236
C 21	14	93.3	3135	US-09-321-276-1
C 22	14	93.3	3135	US-09-321-276-3
C 23	14	93.3	3135	US-08-916-481-1
C 24	14	93.3	3135	US-08-916-481-4

25	14	93.3	3405	US-09-949-016-2869	Sequence 2869, Ap
26	14	93.3	3825	US-08-737-597-2	Sequence 2, Appli
27	14	93.3	4085	US-09-949-016-469	Sequence 469, App
28	14	93.3	13926	US-08-961-527-5	Sequence 5, Appli
29	14	93.3	25464	US-09-326-480A-4	Sequence 4, Appli
30	14	93.3	34261	US-09-949-016-14611	Sequence 14611, A
31	14	93.3	85368	US-09-949-016-12211	Sequence 12211, A
32	14	93.3	98439	US-09-949-016-13597	Sequence 13597, A
33	14	93.3	360470	US-09-949-016-13173	Sequence 13173, A
34	13.4	89.3	163	US-09-113-294A-700	Sequence 700, App
35	13.4	89.3	188	US-09-513-999C-27410	Sequence 27410, A
36	13.4	89.3	258	US-09-107-433-1851	Sequence 1851, Ap
37	13.4	89.3	601	US-09-949-016-33580	Sequence 33580, A
38	13.4	89.3	601	US-09-949-016-33581	Sequence 33581, A
39	13.4	89.3	601	US-09-949-016-48061	Sequence 48061, A
40	13.4	89.3	601	US-09-949-016-68083	Sequence 68083, A
41	13.4	89.3	601	US-09-949-016-80541	Sequence 80541, A
42	13.4	89.3	601	US-09-949-016-80542	Sequence 80542, A
43	13.4	89.3	601	US-09-949-016-83198	Sequence 83198, A
44	13.4	89.3	601	US-09-949-016-83290	Sequence 83290, A
45	13.4	89.3	601	US-09-949-016-122281	Sequence 122281, A
46	13.4	89.3	601	US-09-949-016-128690	Sequence 128690, A
47	13.4	89.3	601	US-09-949-016-129009	Sequence 129009, A
48	13.4	89.3	601	US-09-949-016-159901	Sequence 159901, A
49	13.4	89.3	601	US-09-949-016-189468	Sequence 189468, A
50	13.4	89.3	601	US-09-949-016-193552	Sequence 193552, A
51	13.4	89.3	601	US-09-949-016-196236	Sequence 196236, A
52	13.4	89.3	601	US-09-949-016-196237	Sequence 196237, A
53	13.4	89.3	601	US-09-949-016-196716	Sequence 196716, A
54	13.4	89.3	601	US-09-949-008-8884	Sequence 8884, Ap
55	13.4	89.3	601	US-09-949-008-8885	Sequence 8885, Ap
56	13.4	89.3	601	US-09-949-002-8886	Sequence 8886, Ap
57	13.4	89.3	659	US-09-533-559-7125	Sequence 7125, Ap
58	13.4	89.3	795	US-09-533-559-1918	Sequence 1918, Ap
59	13.4	89.3	1167	US-09-134-001C-983	Sequence 983, App
60	13.4	89.3	1617	US-09-413-304-8	Sequence 8, Appli
61	13.4	89.3	1617	US-09-817-856-8	Sequence 8, Appli
62	13.4	89.3	1718	US-09-215-450-17	Sequence 17, Appl
63	13.4	89.3	1890	US-09-248-796A-1325	Sequence 1325, Ap
64	13.4	89.3	2061	US-09-653-839-7	Sequence 7, Appli
65	13.4	89.3	2061	US-10-202-619-7	Sequence 7, Appli
66	13.4	89.3	2109	US-09-653-839-5	Sequence 5, Appli
67	13.4	89.3	2109	US-10-202-619-5	Sequence 5, Appli
68	13.4	89.3	2172	US-09-653-839-3	Sequence 3, Appli
69	13.4	89.3	2172	US-10-202-619-3	Sequence 3, Appli
70	13.4	89.3	2220	US-09-653-839-1	Sequence 1, Appli
71	13.4	89.3	2220	US-10-202-619-1	Sequence 1, Appli
72	13.4	89.3	2341	US-09-949-016-4080	Sequence 4080, Ap
73	13.4	89.3	2387	US-08-961-527-56	Sequence 56, Appl
74	13.4	89.3	2492	US-09-949-016-5560	Sequence 5560, Ap
75	13.4	89.3	2806	US-09-653-839-9	Sequence 9, Appli
76	13.4	89.3	2806	US-10-202-619-9	Sequence 9, Appli
77	13.4	89.3	2817	US-10-104-047-1687	Sequence 1687, Ap
78	13.4	89.3	3250	US-09-949-016-800	Sequence 800, App
79	13.4	89.3	3754	US-09-561-709B-6	Sequence 6, Appli
80	13.4	89.3	3818	US-09-949-016-5445	Sequence 5445, Ap
81	13.4	89.3	4286	US-09-413-304-7	Sequence 7, Appli
82	13.4	89.3	4286	US-08-817-856-7	Sequence 7, Appli
83	13.4	89.3	4289	US-09-949-016-627	Sequence 627, App
84	13.4	89.3	5874	US-09-561-709B-2	Sequence 2, Appli
85	13.4	89.3	10106	US-09-949-016-17187	Sequence 17187, A
86	13.4	89.3	11667	US-09-949-016-13934	Sequence 13934, A
87	13.4	89.3	14565	US-09-949-016-16620	Sequence 16620, A
88	13.4	89.3	18471	US-09-949-016-14288	Sequence 14288, A
89	13.4	89.3	25190	US-09-949-016-15906	Sequence 15906, A
90	13.4	89.3	25559	US-09-949-016-16707	Sequence 16707, A
91	13.4	89.3	27120	US-09-949-016-15822	Sequence 15822, A
92	13.4	89.3	27120	US-09-949-016-16210	Sequence 16210, A
93	13.4	89.3	27933	US-09-949-016-12369	Sequence 12369, A
94	13.4	89.3	29569	US-09-949-016-15875	Sequence 15875, A
95	13.4	89.3	29960	US-09-949-016-11978	Sequence 11978, A
96	13.4	89.3	30054	US-09-949-016-16100	Sequence 16100, A
97	13.4	89.3	30291	US-09-949-016-12875	Sequence 12875, A

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:15:47 ; Search time 282 Seconds  
(without alignments)  
116.622 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 attcaaaagagcaa 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications\_NA\_New.\*

- 1: /cgn2\_6/prodata/2/pubnpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/prodata/2/pubnpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/2/pubnpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/2/pubnpna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/prodata/2/pubnpna/US05\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/prodata/2/pubnpna/US09\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/prodata/2/pubnpna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/prodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/prodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/prodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/prodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/2/pubnpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	93.3	25	12	US-11-136-527-110483
C 2	14	93.3	25	12	US-11-136-527-110485
C 3	14	93.3	25	12	US-11-136-527-110492
C 4	14	93.3	25	12	US-11-136-527-110503
C 5	14	93.3	25	12	US-11-136-527-110504
C 6	14	93.3	25	12	US-11-136-527-110505
C 7	14	93.3	25	12	US-11-136-527-110514
C 8	14	93.3	25	12	US-11-136-527-110514
C 9	14	93.3	25	12	US-11-136-527-112762
C 10	14	93.3	25	12	US-11-136-527-312778
C 11	14	93.3	25	12	US-11-136-527-312780
C 12	14	93.3	25	12	US-11-136-527-312781
C 13	14	93.3	25	12	US-11-136-527-312785
C 14	14	93.3	25	12	US-11-136-527-312789
C 15	14	93.3	429	6	US-09-925-065A-95610
C 16	14	93.3	520	6	US-09-925-065A-404803
C 17	14	93.3	543	6	US-09-925-065A-340164
C 18	14	93.3	559	6	US-09-925-065A-156850
C 19	14	93.3	587	6	US-09-925-065A-457748
C 20	14	93.3	600	12	US-11-136-527-6628
					Sequence 6628, Ap
					Sequence 835726,

21	14	93.3	611	6	US-09-925-065A-383746	Sequence 383746,
22	14	93.3	611	6	US-09-925-065A-383747	Sequence 383747,
23	14	93.3	611	6	US-09-925-065A-383748	Sequence 383748,
C 24	14	93.3	680	6	US-09-925-065A-596124	Sequence 596124,
C 25	14	93.3	686	6	US-09-925-065A-884458	Sequence 884458,
C 26	14	93.3	748	6	US-09-925-065A-947300	Sequence 947300,
C 27	14	93.3	753	6	US-09-925-065A-947492	Sequence 947492,
C 28	14	93.3	991	6	US-09-925-065A-2135	Sequence 2135, Ap
29	14	93.3	1045	8	US-10-750-185-44511	Sequence 44511, A
30	14	93.3	1045	8	US-10-750-185-44511	Sequence 44511, A
31	14	93.3	1072	8	US-10-750-185-35917	Sequence 35917, A
32	14	93.3	1072	8	US-10-750-185-35917	Sequence 35917, A
C 33	14	93.3	1522	8	US-10-750-185-43114	Sequence 43114, A
C 34	14	93.3	1522	8	US-10-750-185-43114	Sequence 43114, A
C 35	14	93.3	1564	8	US-10-750-185-60041	Sequence 60041, A
36	14	93.3	1564	8	US-10-750-185-60041	Sequence 60041, A
37	14	93.3	1685	8	US-10-750-185-64640	Sequence 64640, A
38	14	93.3	1685	8	US-10-750-185-64640	Sequence 64640, A
C 39	14	93.3	1692	8	US-10-873-528-235	Sequence 235, App
C 40	14	93.3	1692	8	US-10-873-528-235	Sequence 235, App
41	14	93.3	1805	8	US-10-750-185-39400	Sequence 39400, A
42	14	93.3	1805	8	US-10-750-185-39400	Sequence 39400, A
43	14	93.3	1937	8	US-10-750-185-59151	Sequence 59151, A
44	14	93.3	1937	8	US-10-750-185-59151	Sequence 59151, A
45	14	93.3	2280	8	US-10-750-185-35996	Sequence 35996, A
46	14	93.3	2280	8	US-10-750-185-35996	Sequence 35996, A
C 47	14	93.3	4378	12	US-11-136-527-2532	Sequence 2532, Ap
C 48	14	93.3	170837	12	US-11-121-086-97	Sequence 97, Appl
49	14	93.3	403278	12	US-10-995-561-13421	Sequence 13421, A
50	13.4	89.3	25	12	US-11-121-849-532232	Sequence 532232,
51	13.4	89.3	25	12	US-11-121-849-532233	Sequence 532233,
C 52	13.4	89.3	50	12	US-11-175-859-2668	Sequence 2668, Ap
53	13.4	89.3	50	12	US-11-175-859-2668	Sequence 2668, Ap
C 54	13.4	89.3	201	8	US-10-995-561-30308	Sequence 30308, A
C 55	13.4	89.3	201	8	US-10-995-561-61782	Sequence 61782, A
56	13.4	89.3	201	8	US-10-995-561-77745	Sequence 77745, A
57	13.4	89.3	411	6	US-09-925-065A-189701	Sequence 189701,
58	13.4	89.3	411	6	US-09-925-065A-189702	Sequence 189702,
59	13.4	89.3	445	6	US-09-925-065A-146934	Sequence 146934,
C 60	13.4	89.3	471	6	US-09-925-065A-227031	Sequence 227031,
C 61	13.4	89.3	474	6	US-09-925-065A-409257	Sequence 409257,
C 62	13.4	89.3	474	6	US-09-925-065A-501244	Sequence 501244,
C 63	13.4	89.3	483	6	US-09-925-065A-470985	Sequence 470985,
C 64	13.4	89.3	493	6	US-09-925-065A-806810	Sequence 806810,
65	13.4	89.3	493	6	US-09-925-065A-535625	Sequence 535625,
C 66	13.4	89.3	501	6	US-09-925-065A-802293	Sequence 802293,
C 67	13.4	89.3	506	6	US-09-925-065A-802397	Sequence 802397,
68	13.4	89.3	506	6	US-09-925-065A-284881	Sequence 284881,
C 69	13.4	89.3	510	6	US-09-925-065A-284882	Sequence 284882,
C 70	13.4	89.3	510	6	US-09-925-065A-802639	Sequence 802639,
C 71	13.4	89.3	510	6	US-09-925-065A-159739	Sequence 159739,
C 72	13.4	89.3	511	6	US-09-925-065A-771812	Sequence 771812,
C 73	13.4	89.3	526	6	US-09-925-065A-288917	Sequence 288917,
74	13.4	89.3	530	6	US-09-925-065A-288918	Sequence 288918,
75	13.4	89.3	530	6	US-09-925-065A-288919	Sequence 288919,
C 76	13.4	89.3	530	6	US-09-925-065A-478261	Sequence 478261,
C 77	13.4	89.3	533	6	US-09-925-065A-629995	Sequence 629995,
C 78	13.4	89.3	537	6	US-09-925-065A-579688	Sequence 579688,
C 79	13.4	89.3	539	6	US-09-925-065A-579689	Sequence 579689,
C 80	13.4	89.3	543	6	US-09-925-065A-233306	Sequence 233306,
C 81	13.4	89.3	543	6	US-09-925-065A-789644	Sequence 789644,
C 82	13.4	89.3	549	6	US-09-925-065A-268015	Sequence 268015,
C 83	13.4	89.3	549	6	US-09-925-065A-658604	Sequence 658604,
C 84	13.4	89.3	554	6	US-09-925-065A-627171	Sequence 627171,
C 85	13.4	89.3	554	6	US-09-925-065A-486215	Sequence 486215,
C 86	13.4	89.3	557	6	US-09-925-065A-563062	Sequence 563062,
C 87	13.4	89.3	557	6	US-09-925-065A-620462	Sequence 620462,
C 88	13.4	89.3	561	6	US-09-925-065A-86845	Sequence 86845, A
C 89	13.4	89.3	563	6	US-09-925-065A-379915	Sequence 379915,
C 90	13.4	89.3	563	6	US-09-925-065A-379916	Sequence 379916,
C 91	13.4	89.3	563	6	US-09-925-065A-695139	Sequence 695139,
C 92	13.4	89.3	563	6		
C 93	13.4	89.3	563	6		

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:41:34 ; Search time 1705.5 Seconds  
(without alignments)  
411.496 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15  
Sequence: 1 attcctaaggagca 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hic:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	129	3	BQ225964 AGENCOURT
2	15	100.0	179	1	AI071880 UI-R-C2-n
3	15	100.0	184	6	CF497100 MG1-0002T
4	15	100.0	203	1	AV371778 AV371778
5	15	100.0	310	7	CR465098 CR465098
6	15	100.0	317	1	AV559947 AV559947
7	15	100.0	363	9	BZ207934 CH230-279
8	15	100.0	367	3	BP629892 BP629892
9	15	100.0	382	3	BP638044 BP638044
10	15	100.0	391	1	AV566547 AV566547
11	15	100.0	402	3	BP661855 BP661855
12	15	100.0	408	8	CX714140 R7PQ1.18
13	15	100.0	416	3	BI298573 UI-R-CV2-
14	15	100.0	417	1	AA487404 aa487404
15	15	100.0	421	3	BP624041 BP624041
16	15	100.0	422	3	BP644816 BP644816
17	15	100.0	433	1	AI071117 UI-R-C2-m
18	15	100.0	435	3	BP786806 BP786806
19	15	100.0	437	7	CV504339 70872.1 M
20	15	100.0	439	10	CW762695 OG_BBA007
21	15	100.0	445	5	BY059558 BY059558
22	15	100.0	446	7	CO242653 WS0031.B2

23	15	100.0	453	3	BP029150 BP029150
24	15	100.0	482	1	AW869926 NXNV.120
25	15	100.0	499	1	AW226640 um57h10.Y
26	15	100.0	505	2	BI071384 C056P77U
27	15	100.0	505	7	CN996996 Mdfw2043e
28	15	100.0	531	9	AZ556227 RPCI-23-1
29	15	100.0	554	1	AV769071 AV769071
30	15	100.0	561	7	CO250585 WS00811.B
31	15	100.0	563	10	CW513658 115 5 105
32	15	100.0	576	5	BX519784 BX519784
33	15	100.0	578	3	BJ559482 BJ559482
34	15	100.0	581	7	CK119279 218f21.PI
35	15	100.0	581	8	DR573692 WS00735.B
36	15	100.0	594	3	BI296694 UI-R-CV2-
37	15	100.0	594	7	CN997689 Mdfw2053m
38	15	100.0	594	9	AQ770337 HS 5333 A
39	15	100.0	611	8	DR090991 RTA1.18
40	15	100.0	615	9	AQ725411 HS 5383 A
41	15	100.0	619	10	CW099364 104 466 1
42	15	100.0	628	7	CO244209 WS0037.B2
43	15	100.0	635	6	CB576979 AMGNNUC:U
44	15	100.0	637	9	BH361278 CH230-107
45	15	100.0	639	2	BB660768 BB660768
46	15	100.0	640	8	DR039899 BNS000032
47	15	100.0	645	9	CE127819 tigr-gss-
48	15	100.0	660	9	BH310733 CH230-129
49	15	100.0	663	1	AV782367 AV782367
50	15	100.0	673	10	AG066816 Pan trogl
51	15	100.0	676	1	AI812975 2C10 Pine
52	15	100.0	681	10	CE810128 tigr-gss-
53	15	100.0	691	11	CR000641 Reverse s
54	15	100.0	694	10	CW300712 104 784 1
55	15	100.0	697	1	AI919923 1453-Pine
56	15	100.0	703	9	CE060510 tigr-gss-
57	15	100.0	706	7	CN203794 Tor4031 G
58	15	100.0	708	10	CW300711 104 784 1
59	15	100.0	710	9	AZ593911 IM0405010
60	15	100.0	711	10	BX126468 Danio rer
61	15	100.0	714	5	BY720389 BY720389
62	15	100.0	727	9	BH929390 odi02h11.
63	15	100.0	737	6	CA125555 SCRLLR105
64	15	100.0	750	7	CV034980 RTNACU1.1
65	15	100.0	760	8	DN837917 SmoC-1.01
66	15	100.0	776	8	DR930330 EST112186
67	15	100.0	801	2	BG619554 602618946
68	15	100.0	822	9	BH703094 BOMNT43TF
69	15	100.0	828	1	AI920097 1627 Pine
70	15	100.0	834	8	DR579405 WS00751.C
71	15	100.0	840	6	CA492067 AGENCOURT
72	15	100.0	848	9	AQ751802 HS 5569 B
73	15	100.0	848	9	BZ117704 CH230-510
74	15	100.0	857	10	C2976585 178493 To
75	15	100.0	873	1	AJ816505 AJ816505
76	15	100.0	892	7	CV198033 CGF100395
77	15	100.0	906	7	CO238814 WS00722.B
78	15	100.0	919	2	BF138968 601784103
79	15	100.0	974	4	BM909843 AGENCOURT
80	15	100.0	1100	3	BM909843 AGENCOURT
81	15	100.0	1144	9	CC240920 CH261-10A
82	15	100.0	1517	2	BG390402 602416026
83	14	93.3	147	7	CK786054 UI-D-GC1-
84	14	93.3	187	3	BI437383 9C59104.Y
85	14	93.3	218	1	AW036723 EST282721
86	14	93.3	221	3	BP877616 BP877616
87	14	93.3	233	9	BZ933187 CH240 88C
88	14	93.3	235	1	AW921146 EST352450
89	14	93.3	235	9	CC515846 CH240 361
90	14	93.3	237	1	AW838779 CM4-LT005
91	14	93.3	243	11	DE091018 Oryzias 1
92	14	93.3	245	1	AA140794 CK01012 5
93	14	93.3	245	3	BI574610 RH25903.5
94	14	93.3	262	1	AA405522 zw39all.1
95	14	93.3	265	2	BE433934 EST405012

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:12:03 ; Search time 401.5 Seconds  
(without alignments)  
308.943 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 attctcaagagagcaa 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	15	8	US-10-804-470-2	Sequence 2, Appli
2	15	100.0	25	7	US-10-719-956-571453	Sequence 571453,
3	15	100.0	43	8	US-10-804-470-3	Sequence 3, Appli
4	15	100.0	43	8	US-10-804-470-5	Sequence 5, Appli
5	15	100.0	43	8	US-10-804-470-6	Sequence 6, Appli
6	15	100.0	43	8	US-10-804-470-7	Sequence 7, Appli
7	15	100.0	43	8	US-10-804-470-8	Sequence 8, Appli
8	15	100.0	1820	7	US-10-437-963-97628	Sequence 97628, A
9	15	100.0	2796	7	US-10-437-963-97626	Sequence 97626, A
10	15	100.0	3335	7	US-10-437-963-97629	Sequence 97629, A
11	14	93.3	25	7	US-10-719-956-93565	Sequence 93565, A
12	14	93.3	41	3	US-09-765-272-389	Sequence 389, App
13	14	93.3	41	10	US-11-106-649-163	Sequence 163, App
14	14	93.3	373	8	US-10-357-930-17159	Sequence 17159, A
15	14	93.3	378	3	US-09-960-352-7429	Sequence 7429, Ap
16	14	93.3	429	4	US-09-925-065A-95610	Sequence 95610, A
17	14	93.3	434	3	US-09-814-353-4767	Sequence 4767, Ap
18	14	93.3	434	3	US-09-814-353-11064	Sequence 11064, A
19	14	93.3	503	8	US-10-357-930-46982	Sequence 46982, A
20	14	93.3	520	4	US-09-925-065A-404803	Sequence 404803,
21	14	93.3	543	4	US-09-925-065A-340164	Sequence 340164,
22	14	93.3	559	4	US-09-925-065A-156850	Sequence 156850,
23	14	93.3	584	9	US-10-972-079-71790	Sequence 71790, A

C 24	14	93.3	585	3	US-09-814-353-17448	Sequence 17448, A
C 25	14	93.3	587	4	US-09-925-065A-457748	Sequence 457748,
C 26	14	93.3	594	5	US-10-027-632-218198	Sequence 218198,
C 27	14	93.3	594	6	US-10-027-632-218198	Sequence 218198,
C 28	14	93.3	603	8	US-10-425-115-106630	Sequence 106630,
C 29	14	93.3	609	4	US-09-925-065A-835726	Sequence 835726,
C 30	14	93.3	610	8	US-10-425-115-44512	Sequence 44512, A
C 31	14	93.3	611	4	US-09-925-065A-383746	Sequence 383746,
C 32	14	93.3	611	4	US-09-925-065A-383747	Sequence 383747,
C 33	14	93.3	611	4	US-09-925-065A-383748	Sequence 383748,
C 34	14	93.3	680	4	US-09-925-065A-596124	Sequence 596124,
C 35	14	93.3	686	4	US-09-925-065A-884458	Sequence 884458,
C 36	14	93.3	748	4	US-09-925-065A-947300	Sequence 947300,
C 37	14	93.3	753	4	US-09-925-065A-947492	Sequence 947492,
C 38	14	93.3	784	3	US-09-765-272-163	Sequence 163, App
C 39	14	93.3	784	10	US-11-106-649-163	Sequence 163, App
C 40	14	93.3	856	8	US-10-425-115-180559	Sequence 180559,
C 41	14	93.3	881	8	US-10-739-930-5348	Sequence 5348, Ap
C 42	14	93.3	991	4	US-09-925-065A-2135	Sequence 2135, Ap
C 43	14	93.3	1116	7	US-10-724-92A-280	Sequence 280, App
C 44	14	93.3	1134	9	US-10-617-320-1717	Sequence 1717, Ap
C 45	14	93.3	1363	8	US-10-425-115-90531	Sequence 90531, A
C 46	14	93.3	1410	3	US-09-828-302-10	Sequence 10, Appli
C 47	14	93.3	1410	7	US-10-764-259-10	Sequence 10, Appli
C 48	14	93.3	1689	8	US-10-472-928-1231	Sequence 1231, Ap
C 49	14	93.3	1692	3	US-09-769-787-235	Sequence 235, App
C 50	14	93.3	1692	3	US-09-769-787-236	Sequence 236, App
C 51	14	93.3	1955	7	US-10-424-599-56749	Sequence 56749, A
C 52	14	93.3	2133	7	US-10-437-963-80549	Sequence 80549, A
C 53	14	93.3	2467	7	US-10-424-599-4901	Sequence 4901, Ap
C 54	14	93.3	2947	7	US-10-437-963-74398	Sequence 74398, A
C 55	14	93.3	2977	8	US-10-425-115-90533	Sequence 90533, A
C 56	14	93.3	3068	8	US-10-739-930-5312	Sequence 5312, Ap
C 57	14	93.3	3135	3	US-09-800-396-1	Sequence 1, Appli
C 58	14	93.3	3135	3	US-09-878-672-1	Sequence 1, Appli
C 59	14	93.3	3135	3	US-09-878-672-1	Sequence 1, Appli
C 60	14	93.3	3135	3	US-09-878-672-1	Sequence 1, Appli
C 61	14	93.3	3164	5	US-10-027-632-112475	Sequence 112475,
C 62	14	93.3	3164	5	US-10-027-632-112476	Sequence 112476,
C 63	14	93.3	3164	5	US-10-027-632-112477	Sequence 112477,
C 64	14	93.3	3164	6	US-10-027-632-112475	Sequence 112475,
C 65	14	93.3	3164	6	US-10-027-632-112476	Sequence 112476,
C 66	14	93.3	3164	6	US-10-027-632-112477	Sequence 112477,
C 67	14	93.3	4008	10	US-11-097-143-27508	Sequence 27508, A
C 68	14	93.3	4085	9	US-10-756-149-2536	Sequence 2536, Ap
C 69	14	93.3	4085	9	US-10-988-192A-1	Sequence 1, Appli
C 70	14	93.3	4174	6	US-10-101-510-408	Sequence 408, App
C 71	14	93.3	4345	9	US-10-450-763-22054	Sequence 22054, A
C 72	14	93.3	4361	7	US-10-152-319A-1729	Sequence 1729, Ap
C 73	14	93.3	5217	10	US-11-097-143-29512	Sequence 29512, A
C 74	14	93.3	5554	6	US-10-101-510-786	Sequence 786, App
C 75	14	93.3	6317	9	US-10-826-448-3	Sequence 3, Appli
C 76	14	93.3	10785	3	US-09-764-878-324	Sequence 324, App
C 77	14	93.3	10785	5	US-10-079-854-324	Sequence 324, App
C 78	14	93.3	13315	3	US-09-764-878-328	Sequence 328, App
C 79	14	93.3	13315	5	US-10-079-854-328	Sequence 328, App
C 80	14	93.3	13926	2	US-08-961-527-5	Sequence 5, Appli
C 81	14	93.3	13926	7	US-10-158-844-5	Sequence 5, Appli
C 82	14	93.3	20261	3	US-09-764-878-325	Sequence 325, App
C 83	14	93.3	20261	5	US-10-079-854-325	Sequence 325, App
C 84	14	93.3	25464	6	US-10-374-228-4	Sequence 325, App
C 85	14	93.3	150351	7	US-10-322-281-453	Sequence 453, App
C 86	14	93.3	185548	5	US-10-175-523-62	Sequence 62, Appl
C 87	14	93.3	185548	10	US-11-099-266-62	Sequence 1095, Ap
C 88	14	93.3	358246	6	US-10-292-798-1095	Sequence 5729, Ap
C 89	14	93.3	403035	7	US-10-741-601-5729	Sequence 4979, Ap
C 90	14	93.3	216298	8	US-10-472-928-4979	Sequence 3, Appli
C 91	13.4	89.3	24	9	US-10-491-449A-3	Sequence 571452,
C 92	13.4	89.3	25	7	US-10-719-956-571452	Sequence 39314,
C 93	13.4	89.3	25	8	US-10-719-900-39314	Sequence 616964,
C 94	13.4	89.3	25	8	US-10-719-900-39314	Sequence 310036,
C 95	13.4	89.3	25	9	US-10-956-157-310036	Sequence 7, Appli
C 96	13.4	89.3	30	6	US-10-281-845A-7	